SEQUENCE LISTING

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Lee, Sug Hyung
Roth, Wilfred
Stenner-Liewen, Frank

<120> Novel Death Domain Proteins

<130> P-LJ 5037

<150> 60/301,889
<151> 2001-06-29

<150> 09/715,893
<151> 2000-11-17

<160> 62

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 210
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (1)...(210)

<400> 1

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ctt tgg gga aga acc act ctg aaa aga gaa gat aaa agc ccg att gcc   48
Leu Trp Gly Arg Thr Thr Leu Lys Arg Glu Asp Lys Ser Pro Ile Ala
 1               5                  10                  15

ccc gag gaa tta gca ctt gtt cac aac ttg agg aaa atg atg aaa aat   96
Pro Glu Glu Leu Ala Leu Val His Asn Leu Arg Lys Met Met Lys Asn
             20                  25                  30

gat tgg cat gga ggc gcc att gtg tcg gct ttg agc cag act ggg tct   144
Asp Trp His Gly Gly Ala Ile Val Ser Ala Leu Ser Gln Thr Gly Ser
         35                  40                  45

ctc ttt aag ccc cgg aaa gcc tat ctg ccc cag gag ttg ctg gga aag   192
Leu Phe Lys Pro Arg Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys
     50                  55                  60

gaa gga ttt gat gcc ctg                                          210
Glu Gly Phe Asp Ala Leu
 65                  70
```

<210> 2
<211> 70
<212> PRT
<213> Homo sapien

<400> 2

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Leu Trp Gly Arg Thr Thr Leu Lys Arg Glu Asp Lys Ser Pro Ile Ala
 1               5                  10                  15
Pro Glu Glu Leu Ala Leu Val His Asn Leu Arg Lys Met Met Lys Asn
            20                  25                  30
Asp Trp His Gly Gly Ala Ile Val Ser Ala Leu Ser Gln Thr Gly Ser
        35                  40                  45
Leu Phe Lys Pro Arg Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys
    50                  55                  60
Glu Gly Phe Asp Ala Leu
65                  70
```

<210> 3
<211> 297
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (1)...(297)

<400> 3

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acc agt ttt gct tat cca gct ata cga tat ctt ctg tat gga gag aag   48
Thr Ser Phe Ala Tyr Pro Ala Ile Arg Tyr Leu Leu Tyr Gly Glu Lys
 1               5                  10                  15

gga aca gga aaa acc cta agt ctt tgc cat gtt att cat ttc tgt gca   96
Gly Thr Gly Lys Thr Leu Ser Leu Cys His Val Ile His Phe Cys Ala
            20                  25                  30

aaa cag gac tgg ctg ata cta cat att cca gat gct cat ctt tgg gtg   144
Lys Gln Asp Trp Leu Ile Leu His Ile Pro Asp Ala His Leu Trp Val
        35                  40                  45

aaa aat tgt cgg gat ctt ctg cag tcc agc tac aac aaa cag cgc ttt   192
Lys Asn Cys Arg Asp Leu Leu Gln Ser Ser Tyr Asn Lys Gln Arg Phe
    50                  55                  60

gat caa cct tta gag gct tca acc tgg ctg aag aat ttc aaa act aca   240
Asp Gln Pro Leu Glu Ala Ser Thr Trp Leu Lys Asn Phe Lys Thr Thr
65                  70                  75                  80

aat gag cgc ttc ctg aac cag ata aaa gtt caa gag aag tat gtc tgg   288
Asn Glu Arg Phe Leu Asn Gln Ile Lys Val Gln Glu Lys Tyr Val Trp
                85                  90                  95

aat aag aga                                                     297
```

Asn Lys Arg

<210> 4
<211> 99
<212> PRT
<213> Homo sapien

<400> 4
Thr Ser Phe Ala Tyr Pro Ala Ile Arg Tyr Leu Leu Tyr Gly Glu Lys
 1   5   10   15
Gly Thr Gly Lys Thr Leu Ser Leu Cys His Val Ile His Phe Cys Ala
            20   25   30
Lys Gln Asp Trp Leu Ile Leu His Ile Pro Asp Ala His Leu Trp Val
        35   40   45
Lys Asn Cys Arg Asp Leu Leu Gln Ser Ser Tyr Asn Lys Gln Arg Phe
    50   55   60
Asp Gln Pro Leu Glu Ala Ser Thr Trp Leu Lys Asn Phe Lys Thr Thr
65   70   75   80
Asn Glu Arg Phe Leu Asn Gln Ile Lys Val Gln Glu Lys Tyr Val Trp
                85   90   95
Asn Lys Arg

<210> 5
<211> 294
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (1)...(294)

<400> 5
aca tat gtg cgc tgc ctc aat gtt gga cta att agg aag ctg tca gat   48
Thr Tyr Val Arg Cys Leu Asn Val Gly Leu Ile Arg Lys Leu Ser Asp
 1   5   10   15

ttt att gat cct caa gaa gga tgg aag aag tta gct gta gct att aaa   96
Phe Ile Asp Pro Gln Glu Gly Trp Lys Lys Leu Ala Val Ala Ile Lys
            20   25   30

aaa cca tct ggt gat gat aga tac aat cag ttt cac ata agg aga ttt   144
Lys Pro Ser Gly Asp Asp Arg Tyr Asn Gln Phe His Ile Arg Arg Phe
        35   40   45

gaa gca tta ctt caa act gga aaa agt ccc act tct gaa tta ctg ttt   192
Glu Ala Leu Leu Gln Thr Gly Lys Ser Pro Thr Ser Glu Leu Leu Phe
    50   55   60

gac tgg ggc acc aca aat tgc aca gtt ggt gat ctt gtg gat ctt ttg   240
Asp Trp Gly Thr Thr Asn Cys Thr Val Gly Asp Leu Val Asp Leu Leu
65   70   75   80

```
atc caa aat gaa ttt ttt gct cct gcg agt ctt ttg ctc cca gat gct   288
Ile Gln Asn Glu Phe Phe Ala Pro Ala Ser Leu Leu Leu Pro Asp Ala
                 85                  90                  95

gtt ccc                                                          294
Val Pro
```

<210> 6
<211> 98
<212> PRT
<213> Homo sapien

<400> 6

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Thr Tyr Val Arg Cys Leu Asn Val Gly Leu Ile Arg Lys Leu Ser Asp
 1               5                  10                  15
Phe Ile Asp Pro Gln Glu Gly Trp Lys Lys Leu Ala Val Ala Ile Lys
            20                  25                  30
Lys Pro Ser Gly Asp Asp Arg Tyr Asn Gln Phe His Ile Arg Arg Phe
        35                  40                  45
Glu Ala Leu Leu Gln Thr Gly Lys Ser Pro Thr Ser Glu Leu Leu Phe
    50                  55                  60
Asp Trp Gly Thr Thr Asn Cys Thr Val Gly Asp Leu Val Asp Leu Leu
65                  70                  75                  80
Ile Gln Asn Glu Phe Phe Ala Pro Ala Ser Leu Leu Leu Pro Asp Ala
                85                  90                  95
Val Pro
```

<210> 7
<211> 303
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (1)...(303)

<400> 7

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tgg gag gag gat gag tgc ctg gac tac tac ggg atg ctg tcg ctt cac   48
Trp Glu Glu Asp Glu Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His
 1               5                  10                  15

cgt atg ttc gag gtg gtg ggc ggg caa ctg acc gag tgc gag ctg gag   96
Arg Met Phe Glu Val Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu
            20                  25                  30

ctc ctg gcc ttt ctg ctg gat gag gct cct ggc gcc gcc gga ggc tta   144
Leu Leu Ala Phe Leu Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu
        35                  40                  45

gcc cgg gcc cgc agc ggc cta gag ctc ctg ctg gag ctg gag cgc cgc   192
```

```
Ala Arg Ala Arg Ser Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg
     50                  55                  60

ggg cag tgc gac gag agc aac ctg cgg ctg ctg ggg caa ctc ctg cgc   240
Gly Gln Cys Asp Glu Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg
 65                  70                  75                  80

gtg ctg gcc cgc cac gac ctg ctg ccg cac ctg gcg cgc aag cgg cgc   288
Val Leu Ala Arg His Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg
                 85                  90                  95

cgg cca gtg tct cca                                              303
Arg Pro Val Ser Pro
            100
```

<210> 8
<211> 101
<212> PRT
<213> Homo sapien

<400> 8

```
Trp Glu Glu Asp Glu Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His
 1               5                  10                  15
Arg Met Phe Glu Val Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu
            20                  25                  30
Leu Leu Ala Phe Leu Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu
        35                  40                  45
Ala Arg Ala Arg Ser Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg
    50                  55                  60
Gly Gln Cys Asp Glu Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg
65                  70                  75                  80
Val Leu Ala Arg His Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg
                85                  90                  95
Arg Pro Val Ser Pro
            100
```

<210> 9
<211> 195
<212> DNA
<213> Chlamydia trachomatis

<220>
<221> CDS
<222> (1)...(195)

<400> 9

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gat ttg tgg aag cag ttt gtg ttt gct cta gga gtt act cca gaa gag   48
Asp Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Thr Pro Glu Glu
 1               5                  10                  15

tta gag gct cat gag cct agt gaa gca gca aaa gcg aaa gta gct act   96
Leu Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr
            20                  25                  30
```

```
ttc atg cgg tgg tgt aca gga gat tct tta gct gca gga gtg gct gct   144
Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala
         35                  40                  45

ttg tat tct tat gag agt caa att cca cgt atc gct aga gag aaa att   192
Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Arg Ile Ala Arg Glu Lys Ile
     50                  55                  60

cgt                                                               195
Arg
 65
```

<210> 10
<211> 65
<212> PRT
<213> Chlamydia trachomatis

<400> 10

```
Asp Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Thr Pro Glu Glu
 1               5                  10                  15
Leu Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr
            20                  25                  30
Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala
        35                  40                  45
Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Arg Ile Ala Arg Glu Lys Ile
    50                  55                  60
Arg
65
```

<210> 11
<211> 213
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(213)

<400> 11

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cag cag cag gag gaa gtc cag cgg ctc ctg atg atg ggt gag cca gcc   48
Gln Gln Gln Glu Glu Val Gln Arg Leu Leu Met Met Gly Glu Pro Ala
 1               5                  10                  15

aag ggc tgg cag gag ctg gca ggc cac ctc ggc tac caa gct gag gct   96
Lys Gly Trp Gln Glu Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala
            20                  25                  30

gtg gaa acc atg gcc tgt gac caa atg cca gcc tat acc ctg cta agg   144
Val Glu Thr Met Ala Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg
         35                  40                  45

aac tgg gct gcc caa gaa ggc aat aga gct acc ctc aga gtg ctg gag   192
```

```
Asn Trp Ala Ala Gln Glu Gly Asn Arg Ala Thr Leu Arg Val Leu Glu
     50                  55                  60

gat gct ctg gct gcc ata ggc                                        213
Asp Ala Leu Ala Ala Ile Gly
 65                  70


<210> 12
<211> 71
<212> PRT
<213> Mus musculus

<400> 12
Gln Gln Gln Glu Glu Val Gln Arg Leu Leu Met Met Gly Glu Pro Ala
 1               5                  10                  15
Lys Gly Trp Gln Glu Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala
            20                  25                  30
Val Glu Thr Met Ala Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg
        35                  40                  45
Asn Trp Ala Ala Gln Glu Gly Asn Arg Ala Thr Leu Arg Val Leu Glu
    50                  55                  60
Asp Ala Leu Ala Ala Ile Gly
65                  70


<210> 13
<211> 1605
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (74)...(1267)

<400> 13
gaattccgcc ggccccaggc agcgtgtgtc ggtcgcctag gctggagaac tagtcctcga 60
ctcacgtgca agg atg atg ctg aaa gga ata aca agg ctt atc tct agg     109
               Met Met Leu Lys Gly Ile Thr Arg Leu Ile Ser Arg
                1               5                  10

atc cat aag ttg gac cct ggg cgt ttt tta cac atg ggg acc cag gct   157
Ile His Lys Leu Asp Pro Gly Arg Phe Leu His Met Gly Thr Gln Ala
         15                  20                  25

cgc caa agc att gct gct cac cta gat aac cag gtt cca gtt gag agt   205
Arg Gln Ser Ile Ala Ala His Leu Asp Asn Gln Val Pro Val Glu Ser
     30                  35                  40

ccg aga gct att tcc cgc acc aat gag aat gac ccg gcc aag cat ggg   253
Pro Arg Ala Ile Ser Arg Thr Asn Glu Asn Asp Pro Ala Lys His Gly
 45                  50                  55                  60

gat cag cac gag ggt cag cac tac aac atc tcc ccc cag gat ttg gag   301
Asp Gln His Glu Gly Gln His Tyr Asn Ile Ser Pro Gln Asp Leu Glu
```

```
                    65                  70                  75

act gta ttt ccc cat ggc ctt cct cct cgc ttt gtg atg cag gtg aag   349
Thr Val Phe Pro His Gly Leu Pro Pro Arg Phe Val Met Gln Val Lys
                80                  85                  90

aca ttc agt gaa gct tgc ctg atg gta agg aaa cca gcc cta gaa ctt   397
Thr Phe Ser Glu Ala Cys Leu Met Val Arg Lys Pro Ala Leu Glu Leu
        95                  100                 105

ctg cat tac ctg aaa aac acc agt ttt gct tat cca gct ata cga tat   445
Leu His Tyr Leu Lys Asn Thr Ser Phe Ala Tyr Pro Ala Ile Arg Tyr
    110                 115                 120

ctt ctg tat gga gag aag gga aca gga aaa acc cta agt ctt tgc cat   493
Leu Leu Tyr Gly Glu Lys Gly Thr Gly Lys Thr Leu Ser Leu Cys His
125                 130                 135                 140

gtt att cat ttc tgt gca aaa cag gac tgg ctg ata cta cat att cca   541
Val Ile His Phe Cys Ala Lys Gln Asp Trp Leu Ile Leu His Ile Pro
                145                 150                 155

gat gct cat ctt tgg gtg aaa aat tgt cgg gat ctt ctg cag tcc agc   589
Asp Ala His Leu Trp Val Lys Asn Cys Arg Asp Leu Leu Gln Ser Ser
            160                 165                 170

tac aac aaa cag cgc ttt gat caa cct tta gag gct tca acc tgg ctg   637
Tyr Asn Lys Gln Arg Phe Asp Gln Pro Leu Glu Ala Ser Thr Trp Leu
        175                 180                 185

aag aat ttc aaa act aca aat gag cgc ttc ctg aac cag ata aaa gtt   685
Lys Asn Phe Lys Thr Thr Asn Glu Arg Phe Leu Asn Gln Ile Lys Val
    190                 195                 200

caa gag aag tat gtc tgg aat aag aga gaa agc act gag aaa ggg agt   733
Gln Glu Lys Tyr Val Trp Asn Lys Arg Glu Ser Thr Glu Lys Gly Ser
205                 210                 215                 220

cct ctg gga gaa gtg gtt gaa cag ggc ata aca cgg gtg agg aac gcc   781
Pro Leu Gly Glu Val Val Glu Gln Gly Ile Thr Arg Val Arg Asn Ala
                225                 230                 235

aca gat gca gtt gga att gtg ctg aaa gag cta aag agg caa agt tct   829
Thr Asp Ala Val Gly Ile Val Leu Lys Glu Leu Lys Arg Gln Ser Ser
            240                 245                 250

ttg ggt atg ttt cac ctc cta gtg gcc gtg gat gga atc aat gct ctt   877
Leu Gly Met Phe His Leu Leu Val Ala Val Asp Gly Ile Asn Ala Leu
        255                 260                 265

tgg gga aga acc act ctg aaa aga gaa gat aaa agc ccg att gcc ccc   925
Trp Gly Arg Thr Thr Leu Lys Arg Glu Asp Lys Ser Pro Ile Ala Pro
    270                 275                 280

gag gaa tta gca ctt gtt cac aac ttg agg aaa atg atg aaa aat gat   973
```

```
Glu Glu Leu Ala Leu Val His Asn Leu Arg Lys Met Met Lys Asn Asp
285                 290                 295                 300

tgg cat gga ggc gcc att gtg tcg gct ttg agc cag act ggg tct ctc   1021
Trp His Gly Gly Ala Ile Val Ser Ala Leu Ser Gln Thr Gly Ser Leu
                305                 310                 315

ttt aag ccc cgg aaa gcc tat ctg ccc cag gag ttg ctg gga aag gaa   1069
Phe Lys Pro Arg Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys Glu
            320                 325                 330

gga ttt gat gcc ctg gat ccc ttt att ccc atc ctg gtt tcc aac tat   1117
Gly Phe Asp Ala Leu Asp Pro Phe Ile Pro Ile Leu Val Ser Asn Tyr
        335                 340                 345

aac cca aag gaa ttt gaa agt tgt att cag tat tat ttg gaa aac aat   1165
Asn Pro Lys Glu Phe Glu Ser Cys Ile Gln Tyr Tyr Leu Glu Asn Asn
    350                 355                 360

tgg ctt caa cat gag aaa gct cct aca gaa gaa ggg aaa aaa gag ctg   1213
Trp Leu Gln His Glu Lys Ala Pro Thr Glu Glu Gly Lys Lys Glu Leu
365                 370                 375                 380

ctg ttc cta agt aac gcg aac ccc tcg ctg ctg gag cgg cac tgt gcc   1261
Leu Phe Leu Ser Asn Ala Asn Pro Ser Leu Leu Glu Arg His Cys Ala
                385                 390                 395

tac ctc taagccaaga tcacagcatg tgaggaagac agtggacatc tgctttatgc    1317
Tyr Leu


tggacccagt aagatgagga agtcgggcag tacacaggaa gaggagccag gcccttgtac 1377
ctatgggatt ggacaggact gcagttggct ctggacctgc attaaaatgg gtttcactgt 1437
gaatgcgtga caataagata ttcccttgtt cctaaaactt tatatcagtt tattggatgt 1497
ggtttttcac atttaagata attatggctc ttttcctaaa aaataaaata tctttctaaa 1557
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa              1605

<210> 14
<211> 398
<212> PRT
<213> Homo sapien

<400> 14
Met Met Leu Lys Gly Ile Thr Arg Leu Ile Ser Arg Ile His Lys Leu
 1               5                  10                  15
Asp Pro Gly Arg Phe Leu His Met Gly Thr Gln Ala Arg Gln Ser Ile
            20                  25                  30
Ala Ala His Leu Asp Asn Gln Val Pro Val Glu Ser Pro Arg Ala Ile
        35                  40                  45
Ser Arg Thr Asn Glu Asn Asp Pro Ala Lys His Gly Asp Gln His Glu
    50                  55                  60
Gly Gln His Tyr Asn Ile Ser Pro Gln Asp Leu Glu Thr Val Phe Pro
65                  70                  75                  80
His Gly Leu Pro Pro Arg Phe Val Met Gln Val Lys Thr Phe Ser Glu
                85                  90                  95
```

```
Ala Cys Leu Met Val Arg Lys Pro Ala Leu Glu Leu Leu His Tyr Leu
            100                 105                 110
Lys Asn Thr Ser Phe Ala Tyr Pro Ala Ile Arg Tyr Leu Leu Tyr Gly
        115                 120                 125
Glu Lys Gly Thr Gly Lys Thr Leu Ser Leu Cys His Val Ile His Phe
    130                 135                 140
Cys Ala Lys Gln Asp Trp Leu Ile Leu His Ile Pro Asp Ala His Leu
145                 150                 155                 160
Trp Val Lys Asn Cys Arg Asp Leu Leu Gln Ser Ser Tyr Asn Lys Gln
                165                 170                 175
Arg Phe Asp Gln Pro Leu Glu Ala Ser Thr Trp Leu Lys Asn Phe Lys
            180                 185                 190
Thr Thr Asn Glu Arg Phe Leu Asn Gln Ile Lys Val Gln Glu Lys Tyr
        195                 200                 205
Val Trp Asn Lys Arg Glu Ser Thr Glu Lys Gly Ser Pro Leu Gly Glu
    210                 215                 220
Val Val Glu Gln Gly Ile Thr Arg Val Arg Asn Ala Thr Asp Ala Val
225                 230                 235                 240
Gly Ile Val Leu Lys Glu Leu Lys Arg Gln Ser Ser Leu Gly Met Phe
                245                 250                 255
His Leu Leu Val Ala Val Asp Gly Ile Asn Ala Leu Trp Gly Arg Thr
            260                 265                 270
Thr Leu Lys Arg Glu Asp Lys Ser Pro Ile Ala Pro Glu Glu Leu Ala
        275                 280                 285
Leu Val His Asn Leu Arg Lys Met Met Lys Asn Asp Trp His Gly Gly
    290                 295                 300
Ala Ile Val Ser Ala Leu Ser Gln Thr Gly Ser Leu Phe Lys Pro Arg
305                 310                 315                 320
Lys Ala Tyr Leu Pro Gln Glu Leu Leu Gly Lys Glu Gly Phe Asp Ala
                325                 330                 335
Leu Asp Pro Phe Ile Pro Ile Leu Val Ser Asn Tyr Asn Pro Lys Glu
            340                 345                 350
Phe Glu Ser Cys Ile Gln Tyr Tyr Leu Glu Asn Asn Trp Leu Gln His
        355                 360                 365
Glu Lys Ala Pro Thr Glu Glu Gly Lys Lys Glu Leu Leu Phe Leu Ser
    370                 375                 380
Asn Ala Asn Pro Ser Leu Leu Glu Arg His Cys Ala Tyr Leu
385                 390                 395
```

<210> 15
<211> 1383
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (1)...(1380)

<400> 15

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atg aac aaa ccc ata aca cca tca aca tat gtg cgc tgc ctc aat gtt   48
Met Asn Lys Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val
 1               5                  10                  15

gga cta att agg aag ctg tca gat ttt att gat cct caa gaa gga tgg   96
```

```
Gly Leu Ile Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp
            20                  25                  30

aag aag tta gct gta gct att aaa aaa cca tct ggt gat gat aga tac   144
Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr
        35                  40                  45

aat cag ttt cac ata agg aga ttt gaa gca tta ctt caa act gga aaa   192
Asn Gln Phe His Ile Arg Arg Phe Glu Ala Leu Leu Gln Thr Gly Lys
    50                  55                  60

agt ccc act tct gaa tta ctg ttt gac tgg ggc acc aca aat tgc aca   240
Ser Pro Thr Ser Glu Leu Leu Phe Asp Trp Gly Thr Thr Asn Cys Thr
65                  70                  75                  80

gtt ggt gat ctt gtg gat ctt ttg atc caa aat gaa ttt ttt gct cct   288
Val Gly Asp Leu Val Asp Leu Leu Ile Gln Asn Glu Phe Phe Ala Pro
                85                  90                  95

gcg agt ctt ttg ctc cca gat gct gtt ccc aaa act gct aat aca cta   336
Ala Ser Leu Leu Leu Pro Asp Ala Val Pro Lys Thr Ala Asn Thr Leu
            100                 105                 110

cct tct aaa gaa gct ata aca gtt cag caa aaa cag atg cct ttc tgt   384
Pro Ser Lys Glu Ala Ile Thr Val Gln Gln Lys Gln Met Pro Phe Cys
        115                 120                 125

gac aaa gac agg aca ttg atg aca cct gtg cag aat ctt gaa caa agc   432
Asp Lys Asp Arg Thr Leu Met Thr Pro Val Gln Asn Leu Glu Gln Ser
    130                 135                 140

tat atg cca cct gac tcc tca agt cca gaa aat aaa agt tta gaa gtt   480
Tyr Met Pro Pro Asp Ser Ser Ser Pro Glu Asn Lys Ser Leu Glu Val
145                 150                 155                 160

agt gat aca cgt ttt cac agt ttt tca ttt tat gaa ttg aag aat gtc   528
Ser Asp Thr Arg Phe His Ser Phe Ser Phe Tyr Glu Leu Lys Asn Val
                165                 170                 175

aca aat aac ttt gat gaa cga ccc att tct gtt ggt ggt aat aaa atg   576
Thr Asn Asn Phe Asp Glu Arg Pro Ile Ser Val Gly Gly Asn Lys Met
            180                 185                 190

gga gag gga gga ttt gga gtt gta tat aaa ggc tac gta aat aac aca   624
Gly Glu Gly Gly Phe Gly Val Val Tyr Lys Gly Tyr Val Asn Asn Thr
        195                 200                 205

act gtg gca gtg aag aag ctt gca gca atg gtt gac att act act gaa   672
Thr Val Ala Val Lys Lys Leu Ala Ala Met Val Asp Ile Thr Thr Glu
    210                 215                 220

gaa ctg aaa cag cag ttt gat caa gaa ata aaa gta atg gca aag tgt   720
Glu Leu Lys Gln Gln Phe Asp Gln Glu Ile Lys Val Met Ala Lys Cys
225                 230                 235                 240
```

```
caa cat gaa aac tta gta gaa cta ctt ggt ttc tca agt gat gga gat      768
Gln His Glu Asn Leu Val Glu Leu Leu Gly Phe Ser Ser Asp Gly Asp
                245                 250                 255

gac ctc tgc tta gta tat gtt tac atg cct aat ggt tca ttg cta gac      816
Asp Leu Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp
            260                 265                 270

aga ctc tct tgc ttg gat ggt act cca cca ctt tct tgg cac atg aga      864
Arg Leu Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg
        275                 280                 285

tgc aag att gct cag ggt gca gct aat ggc atc aat ttt cta cat gaa      912
Cys Lys Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu
    290                 295                 300

aat cat cat att cat aga gat att aaa agt gca aat atc tta ctg gat      960
Asn His His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp
305                 310                 315                 320

gaa gct ttt act gct aaa ata tct gac ttt ggc ctt gca cgg gct tct     1008
Glu Ala Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser
                325                 330                 335

gag aag ttt gcc cag aca gtc atg act agc aga att gtg gga aca aca     1056
Glu Lys Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr
            340                 345                 350

gct tat atg gca cca gaa gct ttg cgt gga gaa ata aca ccc aaa tct     1104
Ala Tyr Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser
        355                 360                 365

gat att tac agc ttt ggt gtg gtt tta cta gaa ata ata act gga ctt     1152
Asp Ile Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu
    370                 375                 380

cca gct gtg gat gaa cac cgt gaa cct cag tta ttg cta gat att aaa     1200
Pro Ala Val Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys
385                 390                 395                 400

gaa gaa att gaa gat gaa gaa aag aca att gaa gat tat att gat aaa     1248
Glu Glu Ile Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Ile Asp Lys
                405                 410                 415

aag atg aat gat gct gat tcc act tca gtt gaa gct atg tac tct gtt     1296
Lys Met Asn Asp Ala Asp Ser Thr Ser Val Glu Ala Met Tyr Ser Val
            420                 425                 430

gct agt caa tgt ctg cat gaa aag aaa aat aag aga cca gac att aag     1344
Ala Ser Gln Cys Leu His Glu Lys Lys Asn Lys Arg Pro Asp Ile Lys
        435                 440                 445

aag gtt caa cag ctg ctg caa gag atg aca gct tct taa                 1383
Lys Val Gln Gln Leu Leu Gln Glu Met Thr Ala Ser
    450                 455                 460
```

<210> 16
<211> 460
<212> PRT
<213> Homo sapien

<400> 16
Met Asn Lys Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val
 1   5   10   15
Gly Leu Ile Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp
            20   25   30
Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr
        35   40   45
Asn Gln Phe His Ile Arg Arg Phe Glu Ala Leu Leu Gln Thr Gly Lys
    50   55   60
Ser Pro Thr Ser Glu Leu Leu Phe Asp Trp Gly Thr Thr Asn Cys Thr
65   70   75   80
Val Gly Asp Leu Val Asp Leu Leu Ile Gln Asn Glu Phe Phe Ala Pro
                85   90   95
Ala Ser Leu Leu Leu Pro Asp Ala Val Pro Lys Thr Ala Asn Thr Leu
            100   105   110
Pro Ser Lys Glu Ala Ile Thr Val Gln Gln Lys Gln Met Pro Phe Cys
        115   120   125
Asp Lys Asp Arg Thr Leu Met Thr Pro Val Gln Asn Leu Glu Gln Ser
    130   135   140
Tyr Met Pro Pro Asp Ser Ser Ser Pro Glu Asn Lys Ser Leu Glu Val
145   150   155   160
Ser Asp Thr Arg Phe His Ser Phe Ser Phe Tyr Glu Leu Lys Asn Val
                165   170   175
Thr Asn Asn Phe Asp Glu Arg Pro Ile Ser Val Gly Gly Asn Lys Met
            180   185   190
Gly Glu Gly Gly Phe Gly Val Val Tyr Lys Gly Tyr Val Asn Asn Thr
        195   200   205
Thr Val Ala Val Lys Lys Leu Ala Ala Met Val Asp Ile Thr Thr Glu
    210   215   220
Glu Leu Lys Gln Gln Phe Asp Gln Glu Ile Lys Val Met Ala Lys Cys
225   230   235   240
Gln His Glu Asn Leu Val Glu Leu Leu Gly Phe Ser Ser Asp Gly Asp
                245   250   255
Asp Leu Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp
            260   265   270
Arg Leu Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg
        275   280   285
Cys Lys Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu
    290   295   300
Asn His His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp
305   310   315   320
Glu Ala Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser
                325   330   335
Glu Lys Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr
            340   345   350
Ala Tyr Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser
        355   360   365
Asp Ile Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu

```
    370                 375                 380
Pro Ala Val Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys
385                 390                 395                 400
Glu Glu Ile Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Ile Asp Lys
                405                 410                 415
Lys Met Asn Asp Ala Asp Ser Thr Ser Val Glu Ala Met Tyr Ser Val
            420                 425                 430
Ala Ser Gln Cys Leu His Glu Lys Lys Asn Lys Arg Pro Asp Ile Lys
        435                 440                 445
Lys Val Gln Gln Leu Leu Gln Glu Met Thr Ala Ser
    450                 455                 460


<210> 17
<211> 1924
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (91)...(1044)

<221> misc_feature
<222> (1)...(1900)
<223> n = A,T,C or G

<400> 17
ccaaaacaag tggctgcggc gtcgcccagg agtcatcgga cgccagaatc tggccgggtt 60
ctgagcttgt tccgcctccc tccccggga atg gcg cta tcc ggg tcg acc ccg  114
                                  Met Ala Leu Ser Gly Ser Thr Pro
                                   1               5

gcc ccg tgc tgg gag gag gat gag tgc ctg gac tac tac ggg atg ctg   162
Ala Pro Cys Trp Glu Glu Asp Glu Cys Leu Asp Tyr Tyr Gly Met Leu
     10                  15                  20

tcg ctt cac cgt atg ttc gag gtg gtg ggc ggg caa ctg acc gag tgc   210
Ser Leu His Arg Met Phe Glu Val Val Gly Gly Gln Leu Thr Glu Cys
 25                  30                  35                  40

gag ctg gag ctc ctg gcc ttt ctg ctg gat gag gct cct ggc gcc gcc   258
Glu Leu Glu Leu Leu Ala Phe Leu Leu Asp Glu Ala Pro Gly Ala Ala
                 45                  50                  55

gga ggc tta gcc cgg gcc cgc agc ggc cta gag ctc ctg ctg gag ctg   306
Gly Gly Leu Ala Arg Ala Arg Ser Gly Leu Glu Leu Leu Leu Glu Leu
             60                  65                  70

gag cgc cgc ggg cag tgc gac gag agc aac ctg cgg ctg ctg ggg caa   354
Glu Arg Arg Gly Gln Cys Asp Glu Ser Asn Leu Arg Leu Leu Gly Gln
         75                  80                  85

ctc ctg cgc gtg ctg gcc cgc cac gac ctg ctg ccg cac ctg gcg cgc   402
Leu Leu Arg Val Leu Ala Arg His Asp Leu Leu Pro His Leu Ala Arg
     90                  95                  100
```

```
aag cgg cgc cgg cca gtg tct cca gaa cgc tat agc tat ggc acc tcc   450
Lys Arg Arg Arg Pro Val Ser Pro Glu Arg Tyr Ser Tyr Gly Thr Ser
105                 110                 115                 120

agc tct tca aag agg aca gag ggt agc tgc cgt cgc cgt cgg cag tca   498
Ser Ser Ser Lys Arg Thr Glu Gly Ser Cys Arg Arg Arg Arg Gln Ser
                125                 130                 135

agc agt tct gca aat tct cag cag ggt cag tgg gag aca ggc tcc ccc   546
Ser Ser Ser Ala Asn Ser Gln Gln Gly Gln Trp Glu Thr Gly Ser Pro
            140                 145                 150

cca acc aag cgg cag cgg cgg agt cgg ggc cgg ccc agt ggt ggt gcc   594
Pro Thr Lys Arg Gln Arg Arg Ser Arg Gly Arg Pro Ser Gly Gly Ala
        155                 160                 165

aga cgg cgg cgg aga ggg gcc cca gcc gca ccc cag cag cag tca gag   642
Arg Arg Arg Arg Arg Gly Ala Pro Ala Ala Pro Gln Gln Gln Ser Glu
    170                 175                 180

ccc gcc aga cct tcc tct gaa ggc aaa gtg acc tgt gac atc cgg ctc   690
Pro Ala Arg Pro Ser Ser Glu Gly Lys Val Thr Cys Asp Ile Arg Leu
185                 190                 195                 200

cgg gtt cga gca gag tac tgc gag cat ggg cca gcc ttg gag cag ggc   738
Arg Val Arg Ala Glu Tyr Cys Glu His Gly Pro Ala Leu Glu Gln Gly
                205                 210                 215

gtg gca tcc cgg cgg ccc cag gcg ctg gcg cgg cag ctg gac gtg ttt   786
Val Ala Ser Arg Arg Pro Gln Ala Leu Ala Arg Gln Leu Asp Val Phe
            220                 225                 230

ggg cag gcc acc gca gtg ctg cgc tca agg gac ctg ggc tct gtg gtt   834
Gly Gln Ala Thr Ala Val Leu Arg Ser Arg Asp Leu Gly Ser Val Val
        235                 240                 245

tgt gac atc aag ttc tca gag ctc tcc tat ctg gac gcc ttc tgg ggc   882
Cys Asp Ile Lys Phe Ser Glu Leu Ser Tyr Leu Asp Ala Phe Trp Gly
    250                 255                 260

gac tac ctg agt ggc gcc ctg ctg cag gcc ctg cgg ggc gtg ttc ctg   930
Asp Tyr Leu Ser Gly Ala Leu Leu Gln Ala Leu Arg Gly Val Phe Leu
265                 270                 275                 280

act gag gcc ctg cga gag gct gtg ggc cgg gag gct gtt cgc ctg ctg   978
Thr Glu Ala Leu Arg Glu Ala Val Gly Arg Glu Ala Val Arg Leu Leu
                285                 290                 295

gtc agt gtg gat gag gct gac tat gag gct ggc cgg cgc cgc ctg ttg   1026
Val Ser Val Asp Glu Ala Asp Tyr Glu Ala Gly Arg Arg Arg Leu Leu
            300                 305                 310

ctg atg gag gag gaa ggg gggcggcgcc cgacagaggc ctcctgatcc          1074
Leu Met Glu Glu Glu Gly
```

315

aggactggca ggattgatcc cacctccaag tctccgggcc accttctcct gggaggacga 1134
ccatctctac ccctagagga ctgtcactct agcatctttg aggactgcga caggaccggg 1194
acagcaggcc ccttgacagc ccctcccaca ggatgtgggc tctgaggcct aaaccatttc 1254
cagctgagtt tccttcccag actcctccta ccccaggtgt gccccattcg cctccggacg 1314
cggcggctgg gcctgtatct cagaagggag gggcacagct acacactcac caaaggcccc 1374
cctgcacatt gtatctctga tcttgggctg tttgcactgt cacaggtgca cacactcgct 1434
catgctcaca ctgcccctgc tgagatcttc ctgggcctct gccctggcct gttcccagca 1494
cacacttttt tggcctaagg gcttctttct caggaccttt aatttgacca ccaacccaaa 1554
ctggggtttc agccaaaatc agtgggcact ggagctgggg tgcacatggg gcctgctcac 1614
cttgcccaca natttccagc cagccagggc cctgcccagc ttcaatttac agacctgact 1674
ntcctcacct tccccccctgc tgtccagagc tgaacataga cttgcacttg gatgtcacct 1734
ggagtgtcac atgggagtgt tatggcagca tcataccaag gcctactgtt gcacatgggg 1794
ccaaaaccag taaacagcca ccttnttgga aagggaatgc aaaggctttg ggggtgatgg 1854
aaaagacctt ttacaaatga taccaattaa actgccctgg aaagggcata ggtgggcaaa 1914
aaaaaaaaaa 1924

<210> 18
<211> 318
<212> PRT
<213> Homo sapien

<400> 18
Met Ala Leu Ser Gly Ser Thr Pro Ala Pro Cys Trp Glu Glu Asp Glu
 1   5   10   15
Cys Leu Asp Tyr Tyr Gly Met Leu Ser Leu His Arg Met Phe Glu Val
            20   25   30
Val Gly Gly Gln Leu Thr Glu Cys Glu Leu Glu Leu Leu Ala Phe Leu
        35   40   45
Leu Asp Glu Ala Pro Gly Ala Ala Gly Gly Leu Ala Arg Ala Arg Ser
    50   55   60
Gly Leu Glu Leu Leu Leu Glu Leu Glu Arg Arg Gly Gln Cys Asp Glu
65   70   75   80
Ser Asn Leu Arg Leu Leu Gly Gln Leu Leu Arg Val Leu Ala Arg His
                85   90   95
Asp Leu Leu Pro His Leu Ala Arg Lys Arg Arg Arg Pro Val Ser Pro
            100   105   110
Glu Arg Tyr Ser Tyr Gly Thr Ser Ser Ser Ser Lys Arg Thr Glu Gly
        115   120   125
Ser Cys Arg Arg Arg Arg Gln Ser Ser Ser Ser Ala Asn Ser Gln Gln
    130   135   140
Gly Gln Trp Glu Thr Gly Ser Pro Pro Thr Lys Arg Gln Arg Arg Ser
145   150   155   160
Arg Gly Arg Pro Ser Gly Gly Ala Arg Arg Arg Arg Arg Gly Ala Pro
                165   170   175
Ala Ala Pro Gln Gln Gln Ser Glu Pro Ala Arg Pro Ser Ser Glu Gly
            180   185   190
Lys Val Thr Cys Asp Ile Arg Leu Arg Val Arg Ala Glu Tyr Cys Glu
        195   200   205
His Gly Pro Ala Leu Glu Gln Gly Val Ala Ser Arg Arg Pro Gln Ala
    210   215   220
Leu Ala Arg Gln Leu Asp Val Phe Gly Gln Ala Thr Ala Val Leu Arg
225   230   235   240
Ser Arg Asp Leu Gly Ser Val Val Cys Asp Ile Lys Phe Ser Glu Leu

```
                245                 250                 255
Ser Tyr Leu Asp Ala Phe Trp Gly Asp Tyr Leu Ser Gly Ala Leu Leu
            260                 265                 270
Gln Ala Leu Arg Gly Val Phe Leu Thr Glu Ala Leu Arg Glu Ala Val
        275                 280                 285
Gly Arg Glu Ala Val Arg Leu Leu Val Ser Val Asp Glu Ala Asp Tyr
    290                 295                 300
Glu Ala Gly Arg Arg Arg Leu Leu Leu Met Glu Glu Glu Gly
305                 310                 315
```

<210> 19
<211> 696
<212> DNA
<213> Chlamydia trachomatis

<220>
<221> CDS
<222> (1)...(693)

<400> 19

```
atg atg gag gtg ttt atg aat ttt tta gat cag tta gat tta att att   48
Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile
 1               5                  10                  15

caa aat aag cat atg cta gaa cac acg ttt tat gtg aaa tgg tcg aag   96
Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
            20                  25                  30

ggg gag ctt act aaa gag caa tta cag gcg tat gcc aaa gac tat tat  144
Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
        35                  40                  45

tta cat atc aaa gcc ttt cct aaa tat tta tct gcg att cat agt cgt  192
Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg
    50                  55                  60

tgc gat gat tta gag gcg cgt aag tta ttg tta gat aac ttg atg gat  240
Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Leu Asp Asn Leu Met Asp
65                  70                  75                  80

gaa gag aac ggt tac cct aat cat att gat ttg tgg aag cag ttt gtg  288
Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val
                85                  90                  95

ttt gct cta gga gtt act cca gaa gag tta gag gct cat gag cct agt  336
Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Glu Pro Ser
            100                 105                 110

gaa gca gca aaa gcg aaa gta gct act ttc atg cgg tgg tgt aca gga  384
Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
        115                 120                 125

gat tct tta gct gca gga gtg gct gct ttg tat tct tat gag agt caa  432
Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
```

```
    130                 135                 140

att cca cgt atc gct aga gag aaa att cgt gga ttg act gag tac ttt   480
Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
145                 150                 155                 160

gga ttt tcc aat cct gaa gac tat gca tat ttc aca gaa cat gaa gaa   528
Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
                165                 170                 175

gcg gat gtg cgg cat gct aga gaa gaa aaa gcg ctc att gag atg ctt   576
Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
            180                 185                 190

ctc aaa gat gac gct gat aaa gtg tta gag gca tcg cag gaa gta acg   624
Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
        195                 200                 205

caa tct ttg tat ggc ttt tta gat tct ttt ttg gat cca cga act tgt   672
Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Arg Thr Cys
    210                 215                 220

tgt agt tgt cat caa tct tat taa                                   696
Cys Ser Cys His Gln Ser Tyr
225                 230
```

<210> 20
<211> 231
<212> PRT
<213> Chlamydia trachomatis

<400> 20

```
Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile
 1               5                  10                  15
Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
            20                  25                  30
Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
        35                  40                  45
Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg
    50                  55                  60
Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Leu Asp Asn Leu Met Asp
65                  70                  75                  80
Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val
                85                  90                  95
Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Glu Pro Ser
            100                 105                 110
Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
        115                 120                 125
Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
    130                 135                 140
Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
145                 150                 155                 160
Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
                165                 170                 175
```

```
Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
            180                 185                 190
Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
        195                 200                 205
Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Arg Thr Cys
    210                 215                 220
Cys Ser Cys His Gln Ser Tyr
225                 230
```

<210> 21
<211> 687
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(684)

<400> 21

```
atg ctt tat aac gtc agc aaa ggt gtg gtc tat tca gat aca gcc ctg   48
Met Leu Tyr Asn Val Ser Lys Gly Val Val Tyr Ser Asp Thr Ala Leu
 1               5                  10                  15

cag ggg cag gac ggg gac agg gaa gga atg tgg gta gga gct ggg gga   96
Gln Gly Gln Asp Gly Asp Arg Glu Gly Met Trp Val Gly Ala Gly Gly
             20                  25                  30

gcc cta gcc ccc aat acc tcc tcc cta ttt ccc cct gag cct cca ggg   144
Ala Leu Ala Pro Asn Thr Ser Ser Leu Phe Pro Pro Glu Pro Pro Gly
         35                  40                  45

gcc tcg agc aac atc att cct gtc tac tgt gct ctc cta gct aca gtg   192
Ala Ser Ser Asn Ile Ile Pro Val Tyr Cys Ala Leu Leu Ala Thr Val
     50                  55                  60

atc ctt ggt ctg ctg gcc tat gtg gcc ttc aaa tgc tgg cgc tca cat   240
Ile Leu Gly Leu Leu Ala Tyr Val Ala Phe Lys Cys Trp Arg Ser His
 65                  70                  75                  80

aag caa agg caa cag ttg gct aaa gct cgg act gta gag cta ggg gac   288
Lys Gln Arg Gln Gln Leu Ala Lys Ala Arg Thr Val Glu Leu Gly Asp
                 85                  90                  95

cct gac agg gac cag agg cgt ggt gac agc aac gtc ttc gtg gac tct   336
Pro Asp Arg Asp Gln Arg Arg Gly Asp Ser Asn Val Phe Val Asp Ser
            100                 105                 110

cct cct agt ctg gag ccc tgt att ccc agc cag gga cca cac ccg gac   384
Pro Pro Ser Leu Glu Pro Cys Ile Pro Ser Gln Gly Pro His Pro Asp
        115                 120                 125

ctt ggc tgc cag ctt tac ctg cat att cca cag cag cag cag gag gaa   432
Leu Gly Cys Gln Leu Tyr Leu His Ile Pro Gln Gln Gln Gln Glu Glu
    130                 135                 140
```

```
gtc cag cgg ctc ctg atg atg ggt gag cca gcc aag ggc tgg cag gag   480
Val Gln Arg Leu Leu Met Met Gly Glu Pro Ala Lys Gly Trp Gln Glu
145                 150                 155                 160

ctg gca ggc cac ctc ggc tac caa gct gag gct gtg gaa acc atg gcc   528
Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala Val Glu Thr Met Ala
                165                 170                 175

tgt gac caa atg cca gcc tat acc ctg cta agg aac tgg gct gcc caa   576
Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg Asn Trp Ala Ala Gln
            180                 185                 190

gaa ggc aat aga gct acc ctc aga gtg ctg gag gat gct ctg gct gcc   624
Glu Gly Asn Arg Ala Thr Leu Arg Val Leu Glu Asp Ala Leu Ala Ala
        195                 200                 205

ata ggc cga gaa gat gtg gtc cag gtt ttg agc tcg cca gct gag agc   672
Ile Gly Arg Glu Asp Val Val Gln Val Leu Ser Ser Pro Ala Glu Ser
    210                 215                 220

tcc tcg gtg gtg tga                                             687
Ser Ser Val Val
225
```

<210> 22
<211> 228
<212> PRT
<213> Mus musculus

<400> 22

```
Met Leu Tyr Asn Val Ser Lys Gly Val Val Tyr Ser Asp Thr Ala Leu
 1               5                  10                  15
Gln Gly Gln Asp Gly Asp Arg Glu Gly Met Trp Val Gly Ala Gly Gly
            20                  25                  30
Ala Leu Ala Pro Asn Thr Ser Ser Leu Phe Pro Pro Glu Pro Pro Gly
        35                  40                  45
Ala Ser Ser Asn Ile Ile Pro Val Tyr Cys Ala Leu Leu Ala Thr Val
    50                  55                  60
Ile Leu Gly Leu Leu Ala Tyr Val Ala Phe Lys Cys Trp Arg Ser His
65                  70                  75                  80
Lys Gln Arg Gln Gln Leu Ala Lys Ala Arg Thr Val Glu Leu Gly Asp
                85                  90                  95
Pro Asp Arg Asp Gln Arg Arg Gly Asp Ser Asn Val Phe Val Asp Ser
            100                 105                 110
Pro Pro Ser Leu Glu Pro Cys Ile Pro Ser Gln Gly Pro His Pro Asp
        115                 120                 125
Leu Gly Cys Gln Leu Tyr Leu His Ile Pro Gln Gln Gln Gln Glu Glu
    130                 135                 140
Val Gln Arg Leu Leu Met Met Gly Glu Pro Ala Lys Gly Trp Gln Glu
145                 150                 155                 160
Leu Ala Gly His Leu Gly Tyr Gln Ala Glu Ala Val Glu Thr Met Ala
                165                 170                 175
Cys Asp Gln Met Pro Ala Tyr Thr Leu Leu Arg Asn Trp Ala Ala Gln
```

```
            180                 185                 190
Glu Gly Asn Arg Ala Thr Leu Arg Val Leu Glu Asp Ala Leu Ala Ala
        195                 200                 205
Ile Gly Arg Glu Asp Val Val Gln Val Leu Ser Ser Pro Ala Glu Ser
    210                 215                 220
Ser Ser Val Val
225
```

<210> 23
<211> 696
<212> DNA
<213> Chlamydia trachomatis

<220>
<221> CDS
<222> (1)...(693)

<400> 23

```
atg atg gag gtg ttt atg aat ttt tta gat cag tta gat tta att att   48
Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile
 1               5                  10                  15

caa aat aag cat atg cta gaa cac aca ttt tat gtg aaa tgg tcg aag   96
Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
            20                  25                  30

ggg gag ctt act aaa gag caa tta cag gcg tat gcc aaa gac tat tat   144
Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
        35                  40                  45

tta cat atc aaa gcc ttt cct aaa tat tta tct gcg att cat agt cgt   192
Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg
    50                  55                  60

tgc gat gat tta gag gcg cgt aag tta ttg tta gat aac ttg atg gat   240
Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Leu Asp Asn Leu Met Asp
65                  70                  75                  80

gaa gag aac ggt tac cct aat cat att gat ttg tgg aag cag ttt gtg   288
Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val
                85                  90                  95

ttt gct cta gga gtt act cca gaa gag tta gag gct cat gag cct agt   336
Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Glu Pro Ser
            100                 105                 110

gaa gca gca aaa gcg aaa gta gct act ttc atg cgg tgg tgt aca gga   384
Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
        115                 120                 125

gat tct tta gct gca gga gtg gct gct ttg tat tct tat gag agt caa   432
Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
    130                 135                 140
```

```
att cca cgt atc gct aga gag aaa att cgt gga ttg act gag tac ttt   480
Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
145                 150                 155                 160

gga ttt tcc aat cct gaa gac tat gca tat ttc aca gaa cat gaa gaa   528
Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
                165                 170                 175

gcg gat gtg cgg cat gct aga gaa gaa aaa gcg ctc att gag atg ctt   576
Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
            180                 185                 190

ctc aaa gat gac gct gat aaa gtg tta gag gca tcg caa gaa gta acg   624
Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
        195                 200                 205

caa tct ttg tat ggc ttt tta gat tct ttt ttg gat cca gga act tgt   672
Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Gly Thr Cys
    210                 215                 220

tgt agt tgt cat caa tct tat taa                                  696
Cys Ser Cys His Gln Ser Tyr
225                 230
```

<210> 24
<211> 231
<212> PRT
<213> Chlamydia trachomatis

<400> 24

```
Met Met Glu Val Phe Met Asn Phe Leu Asp Gln Leu Asp Leu Ile Ile
 1               5                  10                  15
Gln Asn Lys His Met Leu Glu His Thr Phe Tyr Val Lys Trp Ser Lys
            20                  25                  30
Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr
        35                  40                  45
Leu His Ile Lys Ala Phe Pro Lys Tyr Leu Ser Ala Ile His Ser Arg
    50                  55                  60
Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu Leu Asp Asn Leu Met Asp
65                  70                  75                  80
Glu Glu Asn Gly Tyr Pro Asn His Ile Asp Leu Trp Lys Gln Phe Val
                85                  90                  95
Phe Ala Leu Gly Val Thr Pro Glu Glu Leu Glu Ala His Glu Pro Ser
            100                 105                 110
Glu Ala Ala Lys Ala Lys Val Ala Thr Phe Met Arg Trp Cys Thr Gly
        115                 120                 125
Asp Ser Leu Ala Ala Gly Val Ala Ala Leu Tyr Ser Tyr Glu Ser Gln
    130                 135                 140
Ile Pro Arg Ile Ala Arg Glu Lys Ile Arg Gly Leu Thr Glu Tyr Phe
145                 150                 155                 160
Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr Phe Thr Glu His Glu Glu
                165                 170                 175
Ala Asp Val Arg His Ala Arg Glu Glu Lys Ala Leu Ile Glu Met Leu
            180                 185                 190
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Leu Lys Asp Asp Ala Asp Lys Val Leu Glu Ala Ser Gln Glu Val Thr
        195                 200                 205
Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe Leu Asp Pro Gly Thr Cys
    210                 215                 220
Cys Ser Cys His Gln Ser Tyr
225                 230


<210> 25
<211> 211
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (1)...(177)

<400> 25
atg aac aaa ccc ata aca cca tca aca tat gtg cgc tgc ctc aat gtt   48
Met Asn Lys Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val
 1               5                  10                  15

gga cta att agg aag ctg tca gat ttt att gat cct caa gaa gga tgg   96
Gly Leu Ile Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp
             20                  25                  30

aag aag tta gct gta gct att aaa aaa cca tct ggt gat gat aga tac   144
Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr
         35                  40                  45

aat cag ttt cac ata aga tgc tgt tcc caa aac taatacacta ccttctaaag 197
Asn Gln Phe His Ile Arg Cys Cys Ser Gln Asn
     50                  55

aagctataac agtt                                                   211

<210> 26
<211> 59
<212> PRT
<213> Homo sapien

<400> 26
Met Asn Lys Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val
 1               5                  10                  15
Gly Leu Ile Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp
            20                  25                  30
Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr
        35                  40                  45
Asn Gln Phe His Ile Arg Cys Cys Ser Gln Asn
    50                  55


<210> 27
<211> 2817
<212> DNA
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<213> Homo sapien

<220>
<221> CDS
<222> (50)...(1429)

<400> 27
gttcttctgt cgccggcttc agcagcccgc gcccgggcag gaatagaag atg aac aaa 58
                                                    Met Asn Lys
                                                     1

ccc ata aca cca tca aca tat gtg cgc tgc ctc aat gtt gga cta att 106
Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val Gly Leu Ile
     5   10   15

agg aag ctg tca gat ttt att gat cct caa gaa gga tgg aag aag tta 154
Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp Lys Lys Leu
 20   25   30   35

gct gta gct att aaa aaa cca tct ggt gat gat aga tac aat cag ttt 202
Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr Asn Gln Phe
                 40   45   50

cac ata agg aga ttt gaa gca tta ctt caa act gga aaa agt ccc act 250
His Ile Arg Arg Phe Glu Ala Leu Leu Gln Thr Gly Lys Ser Pro Thr
             55   60   65

tct gaa tta ctg ttt gac tgg ggc acc aca aat tgc aca gtt ggt gat 298
Ser Glu Leu Leu Phe Asp Trp Gly Thr Thr Asn Cys Thr Val Gly Asp
         70   75   80

ctt gtg gat ctt ttg atc caa aat gaa ttt ttt gct cct gcg agt ctt 346
Leu Val Asp Leu Leu Ile Gln Asn Glu Phe Phe Ala Pro Ala Ser Leu
     85   90   95

ttg ctc cca gat gct gtt ccc aaa act gct aat aca cta cct tct aaa 394
Leu Leu Pro Asp Ala Val Pro Lys Thr Ala Asn Thr Leu Pro Ser Lys
100   105   110   115

gaa gct ata aca gtt cag caa aaa cag atg cct ttc tgt gac aaa gac 442
Glu Ala Ile Thr Val Gln Gln Lys Gln Met Pro Phe Cys Asp Lys Asp
                120   125   130

agg aca ttg atg aca cct gtg cag aat ctt gaa caa agc tat atg cca 490
Arg Thr Leu Met Thr Pro Val Gln Asn Leu Glu Gln Ser Tyr Met Pro
            135   140   145

cct gac tcc tca agt cca gaa aat aaa agt tta gaa gtt agt gat aca 538
Pro Asp Ser Ser Ser Pro Glu Asn Lys Ser Leu Glu Val Ser Asp Thr
        150   155   160

cgt ttt cac agt ttt tca ttt tat gaa ttg aag aat gtc aca aat aac 586
Arg Phe His Ser Phe Ser Phe Tyr Glu Leu Lys Asn Val Thr Asn Asn
    165   170   175

```
ttt gat gaa cga ccc att tct gtt ggt ggt aat aaa atg gga gag gga     634
Phe Asp Glu Arg Pro Ile Ser Val Gly Gly Asn Lys Met Gly Glu Gly
180                 185                 190                 195

gga ttt gga gtt gta tat aaa ggc tac gta aat aac aca act gtg gca     682
Gly Phe Gly Val Val Tyr Lys Gly Tyr Val Asn Asn Thr Thr Val Ala
                200                 205                 210

gtg aag aag ctt gca gca atg gtt gac att act act gaa gaa ctg aaa     730
Val Lys Lys Leu Ala Ala Met Val Asp Ile Thr Thr Glu Glu Leu Lys
            215                 220                 225

cag cag ttt gat caa gaa ata aaa gta atg gca aag tgt caa cat gaa     778
Gln Gln Phe Asp Gln Glu Ile Lys Val Met Ala Lys Cys Gln His Glu
        230                 235                 240

aac tta gta gaa cta ctt ggt ttc tca agt gat gga gat gac ctc tgc     826
Asn Leu Val Glu Leu Leu Gly Phe Ser Ser Asp Gly Asp Asp Leu Cys
    245                 250                 255

tta gta tat gtt tac atg cct aat ggt tca ttg cta gac aga ctc tct     874
Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp Arg Leu Ser
260                 265                 270                 275

tgc ttg gat ggt act cca cca ctt tct tgg cac atg aga tgc aag att     922
Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg Cys Lys Ile
                280                 285                 290

gct cag ggt gca gct aat ggc atc aat ttt cta cat gaa aat cat cat     970
Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu Asn His His
            295                 300                 305

att cat aga gat att aaa agt gca aat atc tta ctg gat gaa gct ttt     1018
Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp Glu Ala Phe
        310                 315                 320

act gct aaa ata tct gac ttt ggc ctt gca cgg gct tct gag aag ttt     1066
Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser Glu Lys Phe
    325                 330                 335

gcc cag aca gtc atg act agc aga att gtg gga aca aca gct tat atg     1114
Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr Ala Tyr Met
340                 345                 350                 355

gca cca gaa gct ttg cgt gga gaa ata aca ccc aaa tct gat att tac     1162
Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser Asp Ile Tyr
                360                 365                 370

agc ttt ggt gtg gtt tta cta gaa ata ata act gga ctt cca gct gtg     1210
Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu Pro Ala Val
            375                 380                 385

gat gaa cac cgt gaa cct cag tta ttg cta gat att aaa gaa gaa att     1258
Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys Glu Glu Ile
        390                 395                 400
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gaa gat gaa gaa aag aca att gaa gat tat att gat aaa aag atg aat   1306
Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Ile Asp Lys Lys Met Asn
    405                 410                 415

gat gct gat tcc act tca gtt gaa gct atg tac tct ggt gct agc caa   1354
Asp Ala Asp Ser Thr Ser Val Glu Ala Met Tyr Ser Gly Ala Ser Gln
420                 425                 430                 435

tgt cgg cat gaa aag aaa aat aag agc cca gac att aag aag gtt cac   1402
Cys Arg His Glu Lys Lys Asn Lys Ser Pro Asp Ile Lys Lys Val His
                440                 445                 450

cag ctg ctg caa gag atg aca gct tct taaaacttta ttgaaaaaga         1449
Gln Leu Leu Gln Glu Met Thr Ala Ser
            455                 460

ctcttgactt tttatataca cctatctcaa ccatttttt aactgatttt tttcctaaat 1509
attcttcttt acctttaaca aggcataggc tgttgcagga cagtggttat taaagcatgg 1569
gttgaacttc caaaatataa aaatagagcc accatatcaa cacttagccc tacccattag 1629
tatcaccccc agttcttaca gtaatccctg agaaatctcc ttcaagcatc accaaacaca 1689
gtttgaaaat tacagggtta gcaaaaagag cctgggctgt atgtagggtg gaaacactct 1749
gatctgaagc ccagctgact ccactactaa tttgctgtaa agctttggac atacacttag 1809
ctgctgtgag ccactaataa cattgggcta atatctgctg tgcttctctg acaggtagtc 1869
atgaaaatca aatgatgcaa aatatataca agcactttgt aaattgtaaa atgatacaaa 1929
atttaaagtt tatagagcca gttacaaaat cctattagtc atatatttat agattgtgtt 1989
cacagcaatc atttaaccac aaataaaata tcccttgatg atactgccat aatgatatgt 2049
ccattattag attatgttac atgacaaagt tgaaggaatt tggcagatgc agttaaggtt 2109
cctaaacaac tcactttgag actgttgaaa gggcctgacc taatccaagt gaacccctg 2169
caagaagaat tctccttgta agccttgaag aagtatgtga gagggccaca ttggctaaaa 2229
cctaaaggtg gcctctagga gatgagacct accttccagt tgtcagcaag caggaaaaaa 2289
aaattgggac ctcagttgca accacaagga actgaattct gccaaaaatc tgagtcagct 2349
tagaagagta ctccaagctt cagatgataa ccacagcctg ggctgacacc tggatttcag 2409
ctttgcatga tcctcagtat gagaatctat ctgttctgtg ctggacttct aatatataga 2469
actgtgagat aatgggtcac attggctgga tgtggtggct catacctgta aatcccagca 2529
ctttgggagg ccgaggcagg cagatcacct gaggtcaaga gttcaagacc ggcctggcca 2589
acatggtgaa accccgtctc tactaaaaat acaaaaatta gacgagcgtg gtggtggaca 2649
cctgtagtcc cagctgcttg ggaggctgag gcaggagact agctggaacc agggaggtag 2709
aggttgcagt gagctgagat cgtgccactg cactccagcc tgggtgacag agtgagactc 2769
catcataaat aaataaataa ataaatgggt cccattaagc ctttaaaa              2817
```

<210> 28
<211> 460
<212> PRT
<213> Homo sapien

<400> 28

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Met Asn Lys Pro Ile Thr Pro Ser Thr Tyr Val Arg Cys Leu Asn Val
 1               5                  10                  15
Gly Leu Ile Arg Lys Leu Ser Asp Phe Ile Asp Pro Gln Glu Gly Trp
            20                  25                  30
Lys Lys Leu Ala Val Ala Ile Lys Lys Pro Ser Gly Asp Asp Arg Tyr
        35                  40                  45
Asn Gln Phe His Ile Arg Arg Phe Glu Ala Leu Leu Gln Thr Gly Lys
    50                  55                  60
```

Ser Pro Thr Ser Glu Leu Leu Phe Asp Trp Gly Thr Thr Asn Cys Thr
65 70 75 80
Val Gly Asp Leu Val Asp Leu Leu Ile Gln Asn Glu Phe Phe Ala Pro
85 90 95
Ala Ser Leu Leu Leu Pro Asp Ala Val Pro Lys Thr Ala Asn Thr Leu
100 105 110
Pro Ser Lys Glu Ala Ile Thr Val Gln Gln Lys Gln Met Pro Phe Cys
115 120 125
Asp Lys Asp Arg Thr Leu Met Thr Pro Val Gln Asn Leu Glu Gln Ser
130 135 140
Tyr Met Pro Pro Asp Ser Ser Ser Pro Glu Asn Lys Ser Leu Glu Val
145 150 155 160
Ser Asp Thr Arg Phe His Ser Phe Ser Phe Tyr Glu Leu Lys Asn Val
165 170 175
Thr Asn Asn Phe Asp Glu Arg Pro Ile Ser Val Gly Gly Asn Lys Met
180 185 190
Gly Glu Gly Gly Phe Gly Val Val Tyr Lys Gly Tyr Val Asn Asn Thr
195 200 205
Thr Val Ala Val Lys Lys Leu Ala Ala Met Val Asp Ile Thr Thr Glu
210 215 220
Glu Leu Lys Gln Gln Phe Asp Gln Glu Ile Lys Val Met Ala Lys Cys
225 230 235 240
Gln His Glu Asn Leu Val Glu Leu Leu Gly Phe Ser Ser Asp Gly Asp
245 250 255
Asp Leu Cys Leu Val Tyr Val Tyr Met Pro Asn Gly Ser Leu Leu Asp
260 265 270
Arg Leu Ser Cys Leu Asp Gly Thr Pro Pro Leu Ser Trp His Met Arg
275 280 285
Cys Lys Ile Ala Gln Gly Ala Ala Asn Gly Ile Asn Phe Leu His Glu
290 295 300
Asn His His Ile His Arg Asp Ile Lys Ser Ala Asn Ile Leu Leu Asp
305 310 315 320
Glu Ala Phe Thr Ala Lys Ile Ser Asp Phe Gly Leu Ala Arg Ala Ser
325 330 335
Glu Lys Phe Ala Gln Thr Val Met Thr Ser Arg Ile Val Gly Thr Thr
340 345 350
Ala Tyr Met Ala Pro Glu Ala Leu Arg Gly Glu Ile Thr Pro Lys Ser
355 360 365
Asp Ile Tyr Ser Phe Gly Val Val Leu Leu Glu Ile Ile Thr Gly Leu
370 375 380
Pro Ala Val Asp Glu His Arg Glu Pro Gln Leu Leu Leu Asp Ile Lys
385 390 395 400
Glu Glu Ile Glu Asp Glu Glu Lys Thr Ile Glu Asp Tyr Ile Asp Lys
405 410 415
Lys Met Asn Asp Ala Asp Ser Thr Ser Val Glu Ala Met Tyr Ser Gly
420 425 430
Ala Ser Gln Cys Arg His Glu Lys Lys Asn Lys Ser Pro Asp Ile Lys
435 440 445
Lys Val His Gln Leu Leu Gln Glu Met Thr Ala Ser
450 455 460

<210> 29
<211> 142
<212> PRT

<213> Homo sapien

<400> 29

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Lys Leu Lys Gly Glu Pro Gly Trp Val Thr Ile His Gly Met Ala Gly
 1               5                  10                  15
Cys Gly Lys Ser Val Leu Ala Ala Glu Ala Val Arg Asp His Ser Leu
            20                  25                  30
Leu Glu Gly Cys Phe Pro Gly Gly Val His Trp Val Ser Val Gly Lys
        35                  40                  45
Gln Asp Lys Ser Gly Leu Leu Met Lys Leu Gln Asn Leu Cys Thr Arg
    50                  55                  60
Leu Asp Gln Asp Glu Ser Phe Ser Gln Arg Leu Pro Leu Asn Ile Glu
65                  70                  75                  80
Glu Ala Lys Asp Arg Leu Arg Ile Leu Met Leu Arg Lys His Pro Arg
                85                  90                  95
Ser Leu Leu Ile Leu Asp Asp Val Trp Asp Ser Trp Val Leu Lys Ala
            100                 105                 110
Phe Asp Ser Gln Cys Gln Ile Leu Leu Thr Thr Arg Asp Lys Ser Val
        115                 120                 125
Thr Asp Ser Val Met Gly Pro Lys Tyr Val Val Pro Val Glu
    130                 135                 140
```

<210> 30
<211> 145
<212> PRT
<213> C. elegans

<400> 30

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Glu Met Cys Asp Leu Asp Ser Phe Phe Leu Phe Leu His Gly Arg Ala
 1               5                  10                  15
Gly Ser Gly Lys Ser Val Ile Ala Ser Gln Ala Leu Ser Lys Ser Asp
            20                  25                  30
Gln Leu Ile Gly Ile Asn Tyr Asp Ser Ile Val Trp Leu Lys Asp Ser
        35                  40                  45
Gly Thr Ala Pro Lys Ser Thr Phe Asp Leu Phe Thr Asp Ile Leu Leu
    50                  55                  60
Met Leu Lys Ser Glu Asp Asp Leu Leu Asn Phe Pro Ser Val Glu His
65                  70                  75                  80
Val Thr Ser Val Val Leu Lys Arg Met Ile Cys Asn Ala Leu Ile Asp
                85                  90                  95
Arg Pro Asn Thr Leu Phe Val Phe Asp Asp Val Val Gln Glu Glu Thr
            100                 105                 110
Ile Arg Trp Ala Gln Glu Leu Arg Leu Arg Cys Leu Val Thr Thr Arg
        115                 120                 125
Asp Val Glu Ile Ser Asn Ala Ala Ser Gln Thr Cys Glu Phe Ile Glu
    130                 135                 140
Val
145
```

<210> 31
<211> 75
<212> PRT
<213> Homo sapien

<400> 31
Met Asp Phe Ser Arg Asn Leu Tyr Asp Ile Gly Glu Gln Leu Asp Ser
 1   5   10   15
Glu Asp Leu Ala Ser Leu Lys Phe Leu Ser Leu Asp Tyr Ile Pro Gln
            20   25   30
Arg Lys Gln Glu Pro Ile Lys Asp Ala Leu Met Leu Phe Gln Arg Leu
        35   40   45
Gln Glu Lys Arg Met Leu Glu Glu Ser Asn Leu Ser Phe Leu Lys Glu
    50   55   60
Leu Leu Phe Arg Ile Asn Arg Leu Asp Leu Leu
65   70   75

<210> 32
<211> 76
<212> PRT
<213> Homo sapien

<400> 32
His Leu Leu Ile Arg Val Met Leu Tyr Gln Ile Ser Glu Glu Val Ser
 1   5   10   15
Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu Ile Ser
            20   25   30
Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe Ile Glu
        35   40   45
Met Glu Lys Arg Val Ile Leu Gly Glu Gly Lys Leu Asp Ile Leu Lys
    50   55   60
Arg Val Cys Ala Gln Ile Asn Lys Ser Leu Leu Lys
65   70   75

<210> 33
<211> 77
<212> PRT
<213> Homo sapien

<400> 33
Lys Val Ser Phe Arg Glu Lys Leu Leu Ile Ile Asp Ser Asn Leu Gly
 1   5   10   15
Val Gln Asp Val Glu Asn Leu Lys Phe Leu Cys Ile Gly Leu Val Pro
            20   25   30
Asn Lys Lys Leu Glu Lys Ser Ser Ser Ala Ser Asp Val Phe Glu His
        35   40   45
Leu Leu Ala Glu Asp Leu Leu Ser Glu Glu Asp Pro Phe Phe Leu Ala
    50   55   60
Glu Leu Leu Tyr Ile Ile Arg Gln Lys Lys Leu Leu Gln
65   70   75

<210> 34
<211> 72
<212> PRT
<213> Homo sapien

<400> 34
Val Ser Leu Phe Arg Asn Leu Leu Tyr Glu Leu Ser Glu Gly Ile Asp
 1   5   10   15
Ser Glu Asn Leu Lys Asp Met Ile Phe Leu Leu Lys Asp Ser Leu Pro
            20   25   30
Lys Thr Glu Met Thr Ser Leu Ser Phe Leu Ala Phe Leu Glu Lys Gln
        35   40   45
Gly Lys Ile Asp Glu Asp Asn Leu Thr Cys Leu Glu Asp Leu Cys Lys
    50   55   60
Thr Val Val Pro Lys Leu Leu Arg
65   70

<210> 35
<211> 77
<212> PRT
<213> Homo sapien

<400> 35
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
 1   5   10   15
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
            20   25   30
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
        35   40   45
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
    50   55   60
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
65   70   75

<210> 36
<211> 99
<212> PRT
<213> Homo sapien

<400> 36
Trp Pro Glu Glu His Gly Glu Gln Glu His Gly Leu Tyr Ser Leu His
 1   5   10   15
Arg Met Phe Asp Ile Val Gly Thr His Leu Thr His Arg Asp Val Arg
            20   25   30
Val Leu Ser Phe Leu Phe Val Asp Val Ile Asp His Glu Arg Gly Leu
        35   40   45
Ile Arg Asn Gly Arg Asp Phe Leu Leu Ala Leu Glu Arg Gln Gly Arg
    50   55   60
Cys Asp Glu Ser Asn Phe Arg Gln Val Leu Gln Leu Leu Arg Ile Ile
65   70   75   80
Thr Arg His Asp Leu Leu Pro Tyr Val Thr Leu Lys Arg Arg Arg Ala
                85   90   95
Val Cys Pro

<210> 37
<211> 99

<212> PRT
<213> Mus musculus

<400> 37
Trp Pro Glu Glu Arg Gly Glu Gln Glu His Gly Leu Tyr Ser Leu His
 1   5   10   15
Arg Met Phe Asp Ile Val Gly Thr His Leu Thr His Arg Asp Val Arg
            20   25   30
Val Leu Ser Phe Leu Phe Val Asp Val Ile Asp His Glu Arg Gly Leu
        35   40   45
Ile Arg Asn Gly Arg Asp Phe Leu Leu Ala Leu Glu Arg Gln Gly Arg
    50   55   60
Cys Asp Glu Ser Asn Phe Arg Gln Val Leu Gln Leu Leu Arg Ile Ile
65   70   75   80
Thr Arg His Asp Leu Leu Pro Tyr Val Thr Leu Lys Lys Arg Arg Ala
                85   90   95
Val Cys Pro

<210> 38
<211> 146
<212> PRT
<213> Danio rerio

<400> 38
Trp Glu Glu Thr Glu Cys Leu Ser Tyr Tyr Glu Thr Leu Ser Leu His
 1   5   10   15
Glu Ile Phe Glu Ile Val Gly Ser Gln Leu Thr Glu Thr Cys Gly Gly
            20   25   30
Glu Val Ala Phe Leu Leu Asp Glu Thr Tyr Pro Gly Lys His Pro Leu
        35   40   45
Asp Pro Glu Gly Trp Thr Glu Asp Leu Pro Pro Gly Pro Asp Gly Ser
    50   55   60
Pro Gln Ala Asn Thr Pro Cys Pro Arg Leu Leu Lys Ser Trp Gln Arg
65   70   75   80
Met Gln Pro Gln Lys Glu Gly Cys Ser Ile Ala Ser Arg His Arg Pro
                85   90   95
Lys Ser Gly Val Glu Leu Leu Leu Glu Leu Glu Arg Arg Gly Tyr Leu
            100   105   110
Ser Asp Ala Asn Leu Arg Pro Leu Leu Gln Leu Leu Arg Ile Leu Thr
        115   120   125
Arg His Asp Val Leu Pro Phe Val Ser Gln Lys Lys Arg Arg Thr Val
    130   135   140
Ser Pro
145

<210> 39
<211> 82
<212> PRT
<213> Homo sapien

<400> 39
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser

```
 1               5                  10                  15
Ser Ser Glu Leu Thr Glu Leu Lys Tyr Leu Cys Leu Gly Arg Lys Arg
            20                  25                  30
Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met Leu Leu
        35                  40                  45
Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg Glu Leu
    50                  55                  60
Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp Asp Phe
65                  70                  75                  80
Glu Leu
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<210> 40
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 40
atgatgctga aaggaata 18

<210> 41
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 41
agtcctcgac tcacgtgcaa ggatgatgct gaaaggaata 40

<210> 42
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 42
gcgaattcat gaacaaaccc ataacaccat caaca 35

<210> 43
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 43

gcctcgagtt aagaagctgt catctcttgc agcag 35

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 44
atgatggagg tgtttatg 18

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 45
ataagattga tgacaactac 20

<210> 46
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 46
ctccgccgcc gtctgg 16

<210> 47
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 47
cgcccaggag tcatcggacg c 21

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 48

ccgaggtggc ctgccagctc ctg 23

<210> 49
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 49
acacccggac cttgcctgcc agctttac 28

<210> 50
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 50
atgctttata acgtcagc 18

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer

<400> 51
tcacaccacc gaggagctct c 21

<210> 52
<211> 195
<212> DNA
<213> C. muridarum

<220>
<221> CDS
<222> (1)...(195)

<400> 52
gat tta tgg aaa caa ttt gtg ttt gct ctt gga gtg tct tca gaa gag 48
Asp Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu
 1   5   10   15

cta gaa gct cat gaa ccc agt gaa gca gct aaa gct aag gtt gcg aca 96
Leu Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr
            20   25   30

ttt atg cgg tgg tgc aca ggg gat tct tta gca gca gga gta gcg gct 144
Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala

```
         35                  40                  45

ttg tat tct tat gaa agt caa att cct tgc gta gct aaa gaa aaa att   192
Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile
     50                  55                  60

cgt                                                               195
Arg
 65
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<210> 53
<211> 65
<212> PRT
<213> C. muridarum

<400> 53

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Asp Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu
 1               5                  10                  15
Leu Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr
            20                  25                  30
Phe Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala
        35                  40                  45
Leu Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile
    50                  55                  60
Arg
65
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<210> 54
<211> 711
<212> DNA
<213> C. muridarum

<220>
<221> CDS
<222> (1)...(708)

<400> 54

```
atg gaa tca aga aaa gga ata aaa gag gtg agc atg aat ttt tta gat   48
Met Glu Ser Arg Lys Gly Ile Lys Glu Val Ser Met Asn Phe Leu Asp
 1               5                  10                  15

cag cta gat gca att att caa aac aaa cat atg tta gaa cac cct ttt   96
Gln Leu Asp Ala Ile Ile Gln Asn Lys His Met Leu Glu His Pro Phe
            20                  25                  30

tac atg aag tgg tca aaa gga gag ctg aca aaa gaa caa tta cag gca   144
Tyr Met Lys Trp Ser Lys Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala
        35                  40                  45

tac gca aaa gat tac tat ttg cat atc aaa gct ttt cca aaa tat tta   192
Tyr Ala Lys Asp Tyr Tyr Leu His Ile Lys Ala Phe Pro Lys Tyr Leu
     50                  55                  60
```

```
tct gct att cat agc cgt tgt gat gat tta gaa gcc cgc aag tta tta   240
Ser Ala Ile His Ser Arg Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu
 65                  70                  75                  80

tta gat aac tta atg gat gaa gag aat ggt tat cct aat cat att gat   288
Leu Asp Asn Leu Met Asp Glu Glu Asn Gly Tyr Pro Asn His Ile Asp
                 85                  90                  95

tta tgg aaa caa ttt gtg ttt gct ctt gga gtg tct tca gaa gag cta   336
Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu Leu
            100                 105                 110

gaa gct cat gaa ccc agt gaa gca gct aaa gct aag gtt gcg aca ttt   384
Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr Phe
        115                 120                 125

atg cgg tgg tgc aca ggg gat tct tta gca gca gga gta gcg gct ttg   432
Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala Leu
    130                 135                 140

tat tct tat gaa agt caa att cct tgc gta gct aaa gaa aaa att cgt   480
Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile Arg
145                 150                 155                 160

gga ttg att gag tac ttt ggc ttt tct aat cct gaa gat tat gct tat   528
Gly Leu Ile Glu Tyr Phe Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr
                165                 170                 175

ttc acg gag cat gaa gaa gct gat gtg cgt cat gct agg gaa gaa aag   576
Phe Thr Glu His Glu Glu Ala Asp Val Arg His Ala Arg Glu Glu Lys
            180                 185                 190

gcc tta att gag atg ttg tct aga gat gat agc gac aaa gtt tta gaa   624
Ala Leu Ile Glu Met Leu Ser Arg Asp Asp Ser Asp Lys Val Leu Glu
        195                 200                 205

gct tcg cga gaa gtt aca caa tct tta tac ggc ttt ttg gat tca ttt   672
Ala Ser Arg Glu Val Thr Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe
    210                 215                 220

tta gag cct gca aca tgt tgt cat tgt cac aaa gct taa               711
Leu Glu Pro Ala Thr Cys Cys His Cys His Lys Ala
225                 230                 235
```

<210> 55
<211> 236
<212> PRT
<213> C. muridarum

<400> 55

```
Met Glu Ser Arg Lys Gly Ile Lys Glu Val Ser Met Asn Phe Leu Asp
 1               5                  10                  15
Gln Leu Asp Ala Ile Ile Gln Asn Lys His Met Leu Glu His Pro Phe
            20                  25                  30
```

```
Tyr Met Lys Trp Ser Lys Gly Glu Leu Thr Lys Glu Gln Leu Gln Ala
        35                  40                  45
Tyr Ala Lys Asp Tyr Tyr Leu His Ile Lys Ala Phe Pro Lys Tyr Leu
    50                  55                  60
Ser Ala Ile His Ser Arg Cys Asp Asp Leu Glu Ala Arg Lys Leu Leu
65                  70                  75                  80
Leu Asp Asn Leu Met Asp Glu Glu Asn Gly Tyr Pro Asn His Ile Asp
                85                  90                  95
Leu Trp Lys Gln Phe Val Phe Ala Leu Gly Val Ser Ser Glu Glu Leu
            100                 105                 110
Glu Ala His Glu Pro Ser Glu Ala Ala Lys Ala Lys Val Ala Thr Phe
        115                 120                 125
Met Arg Trp Cys Thr Gly Asp Ser Leu Ala Ala Gly Val Ala Ala Leu
    130                 135                 140
Tyr Ser Tyr Glu Ser Gln Ile Pro Cys Val Ala Lys Glu Lys Ile Arg
145                 150                 155                 160
Gly Leu Ile Glu Tyr Phe Gly Phe Ser Asn Pro Glu Asp Tyr Ala Tyr
                165                 170                 175
Phe Thr Glu His Glu Glu Ala Asp Val Arg His Ala Arg Glu Glu Lys
            180                 185                 190
Ala Leu Ile Glu Met Leu Ser Arg Asp Asp Ser Asp Lys Val Leu Glu
        195                 200                 205
Ala Ser Arg Glu Val Thr Gln Ser Leu Tyr Gly Phe Leu Asp Ser Phe
    210                 215                 220
Leu Glu Pro Ala Thr Cys Cys His Cys His Lys Ala
225                 230                 235
```

<210> 56
<211> 65
<212> PRT
<213> C. pneumoniae

<400> 56

```
Asp Leu Trp Arg Gln Phe Ala Leu Ser Leu Gly Val Ser Glu Glu Glu
 1               5                  10                  15
Leu Ala Asn His Glu Phe Ser Gln Ala Ala Gln Asp Met Val Ala Thr
            20                  25                  30
Phe Arg Arg Leu Cys Asp Met Pro Gln Leu Ala Val Gly Leu Gly Ala
        35                  40                  45
Leu Tyr Thr Tyr Glu Ile Gln Ile Pro Gln Val Cys Val Glu Lys Ile
    50                  55                  60
Arg
65
```

<210> 57
<211> 224
<212> PRT
<213> C. pneumoniae

<400> 57

```
Met Thr Ser Trp Ile Glu Leu Leu Asp Lys Gln Ile Glu Asp Gln His
 1               5                  10                  15
Met Leu Lys His Glu Phe Tyr Gln Arg Trp Ser Glu Gly Lys Leu Glu
```

20 25 30
Lys Gln Gln Leu Gln Ala Tyr Ala Lys Asp Tyr Tyr Leu His Ile Lys
35 40 45
Ala Phe Pro Cys Tyr Leu Ser Ala Leu His Ala Arg Cys Asp Asp Leu
50 55 60
Gln Ile Arg Arg Gln Ile Leu Glu Asn Leu Met Asp Glu Glu Ala Gly
65 70 75 80
Asn Pro Asn His Ile Asp Leu Trp Arg Gln Phe Ala Leu Ser Leu Gly
85 90 95
Val Ser Glu Glu Glu Leu Ala Asn His Glu Phe Ser Gln Ala Ala Gln
100 105 110
Asp Met Val Ala Thr Phe Arg Arg Leu Cys Asp Met Pro Gln Leu Ala
115 120 125
Val Gly Leu Gly Ala Leu Tyr Thr Tyr Glu Ile Gln Ile Pro Gln Val
130 135 140
Cys Val Glu Lys Ile Arg Gly Leu Lys Glu Tyr Phe Gly Val Ser Ala
145 150 155 160
Arg Gly Tyr Ala Tyr Phe Thr Val His Gln Glu Ala Asp Ile Lys His
165 170 175
Ala Ser Glu Glu Lys Glu Met Leu Gln Thr Leu Val Gly Arg Glu Asn
180 185 190
Pro Asp Ala Val Leu Gln Gly Ser Gln Glu Val Leu Asp Thr Leu Trp
195 200 205
Asn Phe Leu Ser Ser Phe Ile Asn Ser Thr Glu Pro Cys Ser Cys Lys
210 215 220

<210> 58
<211> 65
<212> PRT
<213> C. psittaci

<400> 58
Asp Leu Trp Lys Asn Phe Ala Tyr Ala Leu Gly Val Thr Glu Glu Glu
1 5 10 15
Leu Glu Asn His Val Pro Ser Ala Ala Ala Gln Lys Lys Val Asp Thr
20 25 30
Phe Leu Arg Trp Cys Thr Gly Asp Ser Leu Ser Ala Gly Val Ala Ala
35 40 45
Leu Tyr Thr Tyr Glu Ser Gln Ile Pro Thr Val Ala Glu Thr Lys Ile
50 55 60
Ser
65

<210> 59
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 59
gcagtcattc gcgttgga 18

<210> 60
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 60
cgcagaacgg gacataactt g 21

<210> 61
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 61
tgatatcgcc gcgctcgtcg tc 22

<210> 62
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 62
ggatggcatg ggggagggca ta 22